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<110> Bougueleret, Lydie

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AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.

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Ser	Asp	Thr	Ala	Pro	Lys	Pro	Asp	Ala	Val	Leu	Lys	Gln	Ala	Phe	Glu		
		235			240					245			250				
cag	gca	ctt	gaa	ttt	cac	aaa	agt	aga	act	att	cct	gct	aac	tggt	aag		1239
Gln	Ala	Leu	Glu	Phe	His	Lys	Ser	Arg	Thr	Ile	Pro	Ala	Asn	Trp	Lys		
			255					260					265				
act	gaa	ttg	aaa	gaa	gat	agc	tct	agc	agt	gaa	gca	gag	gaa	gaa	gag		1287
Thr	Glu	Leu	Lys	Glu	Asp	Ser	Ser	Ser	Ser	Glu	Ala	Glu	Glu	Glu	Glu		
		270					275					280					
gag	gag	gaa	gat	gat	gaa	aaa	gaa	aag	gag	grt	aat	agc	agt	gaa	gaa		1335
Glu	Glu	Glu	Asp	Asp	Glu	Lys	Glu	Lys	Glu	Xaa	Asn	Ser	Ser	Glu	Glu		
		285					290				295						
gar	gaa	gaa	ata	gaa	cca	ttt	cca	gaa	gaa	agg	gag	aac	ttt	ctt	cag		1383
Glu	Glu	Glu	Ile	Glu	Pro	Phe	Pro	Glu	Glu	Arg	Glu	Asn	Phe	Leu	Gln		
		300			305					310							
caa	ttg	tac	aaa	ttt	atg	gaa	gat	aga	ggt	aca	cct	att	aac	aaa	cga		1431
Gln	Leu	Tyr	Lys	Phe	Met	Glu	Asp	Arg	Gly	Thr	Pro	Ile	Asn	Lys	Arg		
		315			320					325				330			
cct	gta	ctt	gga	tat	cga	aat	ttg	aat	ctc	ttt	aag	tta	ttc	aga	ctt		1479
Pro	Val	Leu	Gly	Tyr	Arg	Asn	Leu	Asn	Leu	Phe	Lys	Leu	Phe	Arg	Leu		
			335					340					345				
gta	cac	aaa	ctt	gga	gga	ttt	gat	aat	att	gaa	agt	gga	gct	ggt	tggt		1527
Val	His	Lys	Leu	Gly	Gly	Phe	Asp	Asn	Ile	Glu	Ser	Gly	Ala	Val	Trp		
		350					355					360					
aaa	caa	gtc	tac	caa	gat	ctt	gga	atc	cct	gtc	tta	aat	tca	gct	gca		1575
Lys	Gln	Val	Tyr	Gln	Asp	Leu	Gly	Ile	Pro	Val	Leu	Asn	Ser	Ala	Ala		
		365					370				375						
gga	tac	aat	ggt	aaa	tgt	gct	tat	aaa	aaa	tac	tta	tat	ggt	ttt	gag		1623
Gly	Tyr	Asn	Val	Lys	Cys	Ala	Tyr	Lys	Lys	Tyr	Leu	Tyr	Gly	Phe	Glu		
		380			385					390							
gag	tac	tgt	aga	tca	gcc	aac	att	gaa	ttt	cag	atg	gca	ttg	cca	gag		1671
Glu	Tyr	Cys	Arg	Ser	Ala	Asn	Ile	Glu	Phe	Gln	Met	Ala	Leu	Pro	Glu		
		395			400				405				410				
aaa	ggt	ggt	aac	aag	caa	tgt	aag	gag	tgt	gaa	aat	gta	aaa	gaa	ata		1719
Lys	Val	Val	Asn	Lys	Gln	Cys	Lys	Glu	Cys	Glu	Asn	Val	Lys	Glu	Ile		
			415					420				425					
aaa	ggt	aag	gag	gaa	aat	gaa	aca	gag	atc	aaa	gaa	ata	aag	atg	gag		1767
Lys	Val	Lys	Glu	Glu	Asn	Glu	Thr	Glu	Ile	Lys	Glu	Ile	Lys	Met	Glu		
		430					435				440						
gag	gag	agg	aat	ata	ata	cca	aga	gaa	gaa	aag	cct	att	gag	gat	gaa		1815
Glu	Glu	Arg	Asn	Ile	Ile	Pro	Arg	Glu	Glu	Lys	Pro	Ile	Glu	Asp	Glu		
		445				450					455						
att	gaa	aga	aaa	gaa	aat	att	aag	ccc	tct	ctg	gga	agt	aaa	aag	aat		1863
Ile	Glu	Arg	Lys	Glu	Asn	Ile	Lys	Pro	Ser	Leu	Gly	Ser	Lys	Lys	Asn		

460	tta tta gaa tct ata cct	465	aca cat tct gat cag gaa aaa gaa gtt aac	1911
Leu Leu Glu Ser Ile Pro	Thr His Ser Asp Gln Glu Lys Glu Val Asn			
475	att aaa aaa cca gaa gac aat gaa aat ctg gay gac aaa gat gat gac	480	485	490
Ile Lys Lys Pro Glu Asp	Asn Glu Asn Leu Asp Asp Lys Asp Asp Asp			1959
495	500	505		
aca act agg gta gat gaa tcc ctc aac ata aag gta gaa gct gag gaa	2007			
Thr Thr Arg Val Asp Glu Ser Leu Asn Ile Lys Val Glu Ala Glu Glu				
510	515	520		
gaa aaa gca aaa tct gga gat gaa acg aat aaa gaa gaa gat gaa gat	2055			
Glu Lys Ala Lys Ser Gly Asp Glu Thr Asn Lys Glu Glu Asp Glu Asp				
525	530	535		
gat gaa gaa gca gaa gag gag gag gag gag gaa gaa gaa gaa gag gat	2103			
Asp Glu Glu Ala Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp				
540	545	550		
gaa gat gat gat gac aac aat gag gaa gag gag ttt gag tgc tat cca	2151			
Glu Asp Asp Asp Asp Asn Asn Glu Glu Glu Glu Phe Glu Cys Tyr Pro				
555	560	565	570	
cca ggc atg aaa gtc caa gtg cgg tat gga cga ggg aaa aat caa aaa	2199			
Pro Gly Met Lys Val Gln Val Arg Tyr Gly Arg Gly Lys Asn Gln Lys				
575	580	585		
atg tat gaa gct agt att aaa gat tct gat gtt gaa ggt gga gag gtc	2247			
Met Tyr Glu Ala Ser Ile Lys Asp Ser Asp Val Glu Gly Gly Glu Val				
590	595	600		
ctt tac ttg gtg cat tac tgc gga tgg aat gtg aga tac gat gaa tgg	2295			
Leu Tyr Leu Val His Tyr Cys Gly Trp Asn Val Arg Tyr Asp Glu Trp				
605	610	615		
att aaa gca gat aaa ata gta aga cct gct gat aaa aat gtg cca aag	2343			
Ile Lys Ala Asp Lys Ile Val Arg Pro Ala Asp Lys Asn Val Pro Lys				
620	625	630		
ata aaa cat cgg aag aaa ata aag aat aaa tta gac aaa gaa aaa gac	2391			
Ile Lys His Arg Lys Lys Ile Lys Asn Lys Leu Asp Lys Glu Lys Asp				
635	640	645	650	
aaa gat gaa aaa tac tct cca aaa aac tgt aaa ctt cgg cgc ttg tcc	2439			
Lys Asp Glu Lys Tyr Ser Pro Lys Asn Cys Lys Leu Arg Arg Leu Ser				
655	660	665		
aaa cca cca ttt cag aca aat cca tct cct gaa atg gta tcc aaa ctg	2487			
Lys Pro Pro Phe Gln Thr Asn Pro Ser Pro Glu Met Val Ser Lys Leu				
670	675	680		
gat ctc act gat gcc aaa aac tct gat act gct cat att aag tcc ata	2535			
Asp Leu Thr Asp Ala Lys Asn Ser Asp Thr Ala His Ile Lys Ser Ile				
685	690	695		
gaa att act tcg atc ctt aat gga ctt caa gct tct gaa agt tct gct	2583			
Glu Ile Thr Ser Ile Leu Asn Gly Leu Gln Ala Ser Glu Ser Ser Ala				
700	705	710		
gaa gac agt gag cag gaa gat gag aga ggt gct caa gac atg gat aat	2631			
Glu Asp Ser Glu Gln Glu Asp Glu Arg Gly Ala Gln Asp Met Asp Asn				
715	720	725	730	
aat ggc aaa gag gaa tct aag att gat cat ttg acc aac aac aga aat	2679			
Asn Gly Lys Glu Glu Ser Lys Ile Asp His Leu Thr Asn Asn Arg Asn				
735	740	745		
gat ctt att tca aag gag gaa cag aac agt tca tct ttg cta gaa gaa	2727			
Asp Leu Ile Ser Lys Glu Glu Gln Asn Ser Ser Ser Leu Leu Glu Glu				
750	755	760		
aac aaa gtt cat gca gat ttg gta ata tcc aaa cca gtg tca aaa tct	2775			
Asn Lys Val His Ala Asp Leu Val Ile Ser Lys Pro Val Ser Lys Ser				

cca gaa aga tta agg aaa gat ata gaa gta tta tcc gaa gat act gat	765	770	775	2823
Pro Glu Arg Leu Arg Lys Asp Ile Glu Val Leu Ser Glu Asp Thr Asp				
tat gaa gaa gat gaa gtc aca aaa aag aga aag gat gtc aag aag gac	780	785	790	2871
Tyr Glu Glu Asp Glu Val Thr Lys Lys Arg Lys Asp Val Lys Lys Asp				
aca aca gat aaa tct tca aaa cca caa ata aaa cgt ggt aaa aga agg	800	805	810	2919
Thr Thr Asp Lys Ser Ser Lys Pro Gln Ile Lys Arg Gly Lys Arg Arg				
tat tgc aat aca gaa gag tgt cta aaa act gga tca cct ggc aaa aag	815	820	825	2967
Tyr Cys Asn Thr Glu Glu Cys Leu Lys Thr Gly Ser Pro Gly Lys Lys				
gaa gag aag gcc aag aac aaa gaa tca ctt tgc atg gaa aac agt agc	830	835	840	3015
Glu Glu Lys Ala Lys Asn Lys Glu Ser Leu Cys Met Glu Asn Ser Ser				
aac agc tct tca gat gaa gat gaa gaa gaa aca aaa gca aag atg aca	845	850	855	3063
Asn Ser Ser Ser Asp Glu Asp Glu Glu Glu Thr Lys Ala Lys Met Thr				
cca act aag aaa tac aat ggt ttg gag gaa aaa aga aaa tct cta cgg	860	865	870	3111
Pro Thr Lys Lys Tyr Asn Gly Leu Glu Glu Lys Arg Lys Ser Leu Arg				
aca act ggt ttc tat tca gga ttt tca gaa gtg gca gaa aaa agg att	880	885	890	3159
Thr Thr Gly Phe Tyr Ser Gly Phe Ser Glu Val Ala Glu Lys Arg Ile				
aaa ctt tta aat aac tct gat gaa aga ctt caa aac agc agg gcc aaa	895	900	905	3207
Lys Leu Leu Asn Asn Ser Asp Glu Arg Leu Gln Asn Ser Arg Ala Lys				
gat cga aaa gat gtc tgg tca agt att cag gga cag tgg cct aaa aaa	910	915	920	3255
Asp Arg Lys Asp Val Trp Ser Ser Ile Gln Gly Gln Trp Pro Lys Lys				
acg ctg aaa gag ctt ttt tca gac tct gat act gag gct gca gct tcc	925	930	935	3303
Thr Leu Lys Glu Leu Phe Ser Asp Ser Asp Thr Glu Ala Ala Ala Ser				
cca ccg cat cct gcc cca gag gag grg gtg gca gag gag tca mtg cag	940	945	950	3351
Pro Pro His Pro Ala Pro Glu Glu Xaa Val Ala Glu Glu Ser Xaa Gln				
act gtg gct gaa gag gag agt tgt tca ccc agt gta gaa cta gaa aaa	955	960	965	3399
Thr Val Ala Glu Glu Ser Cys Ser Pro Ser Val Glu Leu Glu Lys				
cca cct cca gtc aat gtc gat agt aaa ccc att gaa gaa aaa aca gta	975	980	985	3447
Pro Pro Pro Val Asn Val Asp Ser Lys Pro Ile Glu Glu Lys Thr Val				
gag gtc aat gac aga aaa gca gaa ttt cca agt agt ggc agt aat tca	990	995	1000	3495
Glu Val Asn Asp Arg Lys Ala Glu Phe Pro Ser Ser Gly Ser Asn Ser				
gtg cta aat acc cct cct act aca cct gaa tcg cct tca tca gtc act	1005	1010	1015	3543
Val Leu Asn Thr Pro Pro Thr Thr Pro Glu Ser Pro Ser Ser Val Thr				
gta aca gaa ggc agc cgg cag cag tct tct gta aca gta tca gaa cca	1020	1025	1030	3591
Val Thr Glu Gly Ser Arg Gln Gln Ser Ser Val Thr Val Ser Glu Pro				
ctg gct cca aac caa gaa gag gtt cga agt atc aag agt gaa act gat	1035	1040	1045	3639
Leu Ala Pro Asn Gln Glu Glu Val Arg Ser Ile Lys Ser Glu Thr Asp				
agc aca att gag gtg gat agt gtt gct ggg gag ctc caa gac ctc cag	1055	1060	1065	3687
Ser Thr Ile Glu Val Asp Ser Val Ala Gly Glu Leu Gln Asp Leu Gln				

tct gaa ggg aat agc tcg cca gca ggt ttt gat gcc agt gtg agc tca	1070	1075	1080	3735
Ser Glu Gly Asn Ser Ser Pro Ala Gly Phe Asp Ala Ser Val Ser Ser				
agc agt agt aat cag cca gaa cca gaa cat cct gaa aaa gcc tgt aca	1085	1090	1095	3783
Ser Ser Ser Asn Gln Pro Glu Pro Glu His Pro Glu Lys Ala Cys Thr				
ggt cag aaa aga gtg aaa gat gct cag gga gga gga agt tca tca aaa	1100	1105	1110	3831
Gly Gln Lys Arg Val Lys Asp Ala Gln Gly Gly Ser Ser Ser Lys				
aag cag aaa aga agc cat aaa gca aca gtg gta aac aac aaa aag aag	1115	1120	1125	3879
Lys Gln Lys Arg Ser His Lys Ala Thr Val Val Asn Asn Lys Lys Lys				
gga aaa ggc aca aat agt agt gat agt gaa gaa ctt tca gct ggt gaa	1135	1140	1145	3927
Gly Lys Gly Thr Asn Ser Ser Asp Ser Glu Glu Leu Ser Ala Gly Glu				
agt ata act aag agt cag cca gtc aaa tca gtt tcc act gga atg aag	1150	1155	1160	3975
Ser Ile Thr Lys Ser Gln Pro Val Lys Ser Val Ser Thr Gly Met Lys				
tct cat agt acc aaa tct ccc gca agg acg cag tct cca gga aaa tgt	1165	1170	1175	4023
Ser His Ser Thr Lys Ser Pro Ala Arg Thr Gln Ser Pro Gly Lys Cys				
gga aag aat ggt gat aag gat cct gat ctc aag gaa ccc agt aat cga	1180	1185	1190	4071
Gly Lys Asn Gly Asp Lys Asp Pro Asp Leu Lys Glu Pro Ser Asn Arg				
tta ccc aaa gtt tac aaa tgg agt ttt cag atg tcg gac ctg gaa aat	1195	1200	1205	4119
Leu Pro Lys Val Tyr Lys Trp Ser Phe Gln Met Ser Asp Leu Glu Asn				
atg aca agt gcc gaa cgc atc aca att ctt caa gaa aaa ctt caa gaa	1215	1220	1225	4167
Met Thr Ser Ala Glu Arg Ile Thr Ile Leu Gln Glu Lys Leu Gln Glu				
atc aga aaa cat tat ctg tca tta aaa tct gaa gta gct tcc att gat	1230	1235	1240	4215
Ile Arg Lys His Tyr Leu Ser Leu Lys Ser Glu Val Ala Ser Ile Asp				
cgg agg aga aag cgt tta aag aag aaa gag aga gaa agt gct gct aca	1245	1250	1255	4263
Arg Arg Arg Lys Arg Leu Lys Lys Lys Glu Arg Glu Ser Ala Ala Thr				
tcc tca tcc tcc tct tca cct tca tcc agt tcc ata aca gct gct gtt	1260	1265	1270	4311
Ser Ser Ser Ser Ser Ser Pro Ser Ser Ser Ser Ile Thr Ala Ala Val				
atg tta act tta gct gaa ccg tca atg tcc agc gca tca caa aat gga	1275	1280	1285	4359
Met Leu Thr Leu Ala Glu Pro Ser Met Ser Ser Ala Ser Gln Asn Gly				
atg tca gtt gag tgc agg tga cagcaggact tgctaaagca ctttgcactt	1295	1300	1305	4410
Met Ser Val Glu Cys Arg *				
aatggctgtt gagggccact ttttttttat actgcacagt ggcacaaaaa aatatcagac	1310			4470
aagcactatt ttatatitaa aaattgtttc ttgacaagct gacttggcac ttaagtgcac				4530
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gaattataac	agttatatatt	ttgtgttttc	ttgtaaatgt	ttctttttccc	ttaaatacacg	5250
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cctctggagg	gcagcgcgat	tgggggccccg	gacctccagt	ccgggggggga	tttttcgctg	180
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gcgggaggag	gaggagccgg	agcctctgcc	tcagcagccg	ctggaccgcc	cgcccttctt	300
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 <211> 80
 <212> DNA
 <213> Homo sapiens

 <400> 10
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 <210> 11
 <211> 92
 <212> DNA
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 <212> DNA
 <213> Homo sapiens

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 tctttcaaag atggaaaatt 80

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 <211> 77
 <212> DNA
 <213> Homo sapiens

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 tgctgtttta aagcaag 77

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<212> DNA

<213> Homo sapiens

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<210> 16

<211> 73

<212> DNA

<213> Homo sapiens

<400> 16

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<211> 95

<212> DNA

<213> Homo sapiens

<400> 17

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<211> 98

<212> DNA

<213> Homo sapiens

<400> 18

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<211> 244

<212> DNA

<213> Homo sapiens

<400> 19

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taaggaggaa	aatgaaacag	agatcaaaga	aataaagatg	gaggaggaga	ggaatataat	180
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<211> 176

<212> DNA

<213> Homo sapiens

<400> 20

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ctatccacca	ggcatgaaa	tccaagtgcg	gtatggacga	gggaaaaatc	aaaaaatgta		180
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<210> 22
 <211> 85
 <212> DNA
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			20					25					30		
Lys	Arg	Leu	Val	Lys	Val	Lys	Val	Thr	Phe	Arg	His	Asp	Ser	Ser	Thr
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Lys	Glu	Lys	Glu	Xaa	Asn	Ser	Ser	Glu	Glu	Glu	Glu	Glu	Ile	Glu	Pro
	290				295						300				
Phe	Pro	Glu	Glu	Arg	Glu	Asn	Phe	Leu	Gln	Gln	Leu	Tyr	Lys	Phe	Met
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Glu	Asp	Arg	Gly	Thr	Pro	Ile	Asn	Lys	Arg	Pro	Val	Leu	Gly	Tyr	Arg
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Thr	Lys	Lys	Arg	Lys	Asp	Val	Lys	Lys	Asp	Thr	Thr	Asp	Lys	Ser	Ser
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Lys	Pro	Gln	Ile	Lys	Arg	Gly	Lys	Arg	Arg	Tyr	Cys	Asn	Thr	Glu	Glu
			820					825					830		
Cys	Leu	Lys	Thr	Gly	Ser	Pro	Gly	Lys	Lys	Glu	Glu	Lys	Ala	Lys	Asn
	835						840					845			
Lys	Glu	Ser	Leu	Cys	Met	Glu	Asn	Ser	Ser	Asn	Ser	Ser	Ser	Asp	Glu
	850					855				860					
Asp	Glu	Glu	Glu	Thr	Lys	Ala	Lys	Met	Thr	Pro	Thr	Lys	Lys	Tyr	Asn
865					870					875					880
Gly	Leu	Glu	Glu	Lys	Arg	Lys	Ser	Leu	Arg	Thr	Thr	Gly	Phe	Tyr	Ser
				885					890					895	
Gly	Phe	Ser	Glu	Val	Ala	Glu	Lys	Arg	Ile	Lys	Leu	Leu	Asn	Asn	Ser
			900					905					910		
Asp	Glu	Arg	Leu	Gln	Asn	Ser	Arg	Ala	Lys	Asp	Arg	Lys	Asp	Val	Trp
		915					920					925			
Ser	Ser	Ile	Gln	Gly	Gln	Trp	Pro	Lys	Lys	Thr	Leu	Lys	Glu	Leu	Phe
	930					935					940				
Ser	Asp	Ser	Asp	Thr	Glu	Ala	Ala	Ala	Ser	Pro	Pro	His	Pro	Ala	Pro
945					950					955					960
Glu	Glu	Xaa	Val	Ala	Glu	Glu	Ser	Xaa	Gln	Thr	Val	Ala	Glu	Glu	Glu
			965						970					975	
Ser	Cys	Ser	Pro	Ser	Val	Glu	Leu	Glu	Lys	Pro	Pro	Pro	Val	Asn	Val
			980					985					990		
Asp	Ser	Lys	Pro	Ile	Glu	Glu	Lys	Thr	Val	Glu	Val	Asn	Asp	Arg	Lys
	995						1000					1005			
Ala	Glu	Phe	Pro	Ser	Ser	Gly	Ser	Asn	Ser	Val	Leu	Asn	Thr	Pro	Pro
	1010					1015					1020				
Thr	Thr	Pro	Glu	Ser	Pro	Ser	Ser	Val	Thr	Val	Thr	Glu	Gly	Ser	Arg
1025					1030					1035					1040
Gln	Gln	Ser	Ser	Val	Thr	Val	Ser	Glu	Pro	Leu	Ala	Pro	Asn	Gln	Glu
				1045					1050					1055	
Glu	Val	Arg	Ser	Ile	Lys	Ser	Glu	Thr	Asp	Ser	Thr	Ile	Glu	Val	Asp

				1060					1065					1070		
Ser	Val	Ala	Gly	Glu	Leu	Gln	Asp	Leu	Gln	Ser	Glu	Gly	Asn	Ser	Ser	
		1075					1080					1085				
Pro	Ala	Gly	Phe	Asp	Ala	Ser	Val	Ser	Ser	Ser	Ser	Ser	Asn	Gln	Pro	
	1090					1095				1100						
Glu	Pro	Glu	His	Pro	Glu	Lys	Ala	Cys	Thr	Gly	Gln	Lys	Arg	Val	Lys	
1105					1110					1115					1120	
Asp	Ala	Gln	Gly	Gly	Gly	Ser	Ser	Ser	Lys	Lys	Gln	Lys	Arg	Ser	His	
				1125					1130					1135		
Lys	Ala	Thr	Val	Val	Asn	Asn	Lys	Lys	Lys	Gly	Lys	Gly	Thr	Asn	Ser	
		1140				1145						1150				
Ser	Asp	Ser	Glu	Glu	Leu	Ser	Ala	Gly	Glu	Ser	Ile	Thr	Lys	Ser	Gln	
	1155					1160						1165				
Pro	Val	Lys	Ser	Val	Ser	Thr	Gly	Met	Lys	Ser	His	Ser	Thr	Lys	Ser	
	1170					1175				1180						
Pro	Ala	Arg	Thr	Gln	Ser	Pro	Gly	Lys	Cys	Gly	Lys	Asn	Gly	Asp	Lys	
1185				1190						1195					1200	
Asp	Pro	Asp	Leu	Lys	Glu	Pro	Ser	Asn	Arg	Leu	Pro	Lys	Val	Tyr	Lys	
			1205					1210						1215		
Trp	Ser	Phe	Gln	Met	Ser	Asp	Leu	Glu	Asn	Met	Thr	Ser	Ala	Glu	Arg	
		1220						1225					1230			
Ile	Thr	Ile	Leu	Gln	Glu	Lys	Leu	Gln	Glu	Ile	Arg	Lys	His	Tyr	Leu	
	1235					1240				1245						
Ser	Leu	Lys	Ser	Glu	Val	Ala	Ser	Ile	Asp	Arg	Arg	Arg	Lys	Arg	Leu	
	1250					1255				1260						
Lys	Lys	Lys	Glu	Arg	Glu	Ser	Ala	Ala	Thr	Ser	Ser	Ser	Ser	Ser	Ser	
1265				1270						1275					1280	
Pro	Ser	Ser	Ser	Ser	Ile	Thr	Ala	Ala	Val	Met	Leu	Thr	Leu	Ala	Glu	
			1285					1290						1295		
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10071179-020702

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<400> 31
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<210> 32
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48

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49

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47

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49

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46

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<210> 63
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<223> complement potential microsequencing oligo 5-140-120.mis2

<400> 63
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47

<210> 64
<211> 48
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<220>
<221> allele
<222> 23
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<220>
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<222> 1..22
<223> potential microsequencing oligo 5-140-348.mis1

<400> 64
ggacttcaag gtaaacataa catcgttctg ttgcatgcaa gtatttga

48

<210> 65
<211> 46
<212> DNA
<213> Homo Sapiens

<220>
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<222> 1..46
<223> polymorphic fragment 5-140-361, variant version of SEQ ID44

<220>
<221> allele
<222> 23
<223> deletion

<220>
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<222> 1..22
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<400> 65
aaacataaca atcgttctgt tgtgcaagta tttgatttta atttat

46

<210> 66
 <211> 47
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<220>
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 <223> polymorphic fragment 5-143-101, variant version of SEQ ID45

<220>
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 <223> base C ; A in SEQ ID45

<220>
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 <223> potential microsequencing oligo 5-143-101.mis1

<220>
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<400> 66
 aggagggggt ggcagaggag tcaactgcaga ctgtggctga agaggag

47

<210> 67
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<220>
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<220>
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 <223> base G ; A in SEQ ID46

<220>
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 <223> potential microsequencing oligo 5-143-84.mis1

<220>
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<400> 67
 accgcacacct gcccagagg aggggggtggc agaggagtca ctgcaga

47

<210> 68
<211> 47
<212> DNA
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<220>
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<223> polymorphic fragment 5-145-24, variant version of SEQ ID47

<220>
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<222> 1..23
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<223> complement potential microsequencing oligo 5-145-24.mis2

<400> 68
tagtaagttc tgtgacaact tatgaatgac ataaagaaca tgtagtt

47

<210> 69
<211> 47
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<220>
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<223> polymorphic fragment 5-148-352, variant version of SEQ ID48

<220>
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<222> 24
<223> base T ; G in SEQ ID48

<220>
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<222> 1..23
<223> potential microsequencing oligo 5-148-352.mis1

<220>
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<223> complement potential microsequencing oligo 5-148-352.mis2

<400> 69
tgcttttccct caagcaataa ttgtttccaa cttgtctggg aattgtg

47

<210> 70

<211> 47
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<220>
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<223> polymorphic fragment 99-1437-325, variant version of SEQ ID49

<220>
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<222> 24
<223> base T ; C in SEQ ID49

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<222> 1..23
<223> potential microsequencing oligo 99-1437-325.mis1

<220>
<221> primer_bind
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<400> 70
caagagctga catttactgc atattttaatt tgtgccgaac actgaac

47

<210> 71
<211> 47
<212> DNA
<213> Homo Sapiens

<220>
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<222> 1..47
<223> polymorphic fragment 99-1442-224, variant version of SEQ ID50

<220>
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<222> 24
<223> base T ; G in SEQ ID50

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<223> potential microsequencing oligo 99-1442-224.mis1

<220>
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<223> complement potential microsequencing oligo 99-1442-224.mis2

<400> 71
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47

<210> 72
<211> 19

<212> DNA
<213> Artificial Sequence

<220>
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<223> upstream amplification primer for SEQ 30, SEQ 51

<400> 72
aaaagaaaac aaacccagg 19

<210> 73
<211> 19
<212> DNA
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<220>
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<223> upstream amplification primer for SEQ 31, SEQ 52

<400> 73
ataagagttt gggaatacc 19

<210> 74
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer for SEQ 32, SEQ 53

<400> 74
tggaaggatg taggatgc 18

<210> 75
<211> 18
<212> DNA
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<220>
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<222> 1..18
<223> upstream amplification primer for SEQ 33, SEQ 54

<400> 75
gctactctgt gtgcaatc 18

<210> 76
<211> 20
<212> DNA
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<220>
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<222> 1..20
 <223> upstream amplification primer for SEQ 34, SEQ 55, SEQ 35, SEQ 56

 <400> 76
 caaacaataa atgtcagtgg 20

 <210> 77
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 <212> DNA
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 <220>
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 <223> upstream amplification primer for SEQ 36, SEQ 57

 <400> 77
 ggttttgaac agcttagtg 19

 <210> 78
 <211> 18
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 <220>
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 <223> upstream amplification primer for SEQ 37, SEQ 58

 <400> 78
 tcttttgagt ctaggacc 18

 <210> 79
 <211> 18
 <212> DNA
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 <220>
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 <223> upstream amplification primer for SEQ 38, SEQ 59, SEQ 39, SEQ 60, SEQ 40, SEQ 61

 <400> 79
 aaagatggag gaggagag 18

 <210> 80
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 <212> DNA
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 <223> upstream amplification primer for SEQ 41, SEQ 62

 <400> 80

tgttgctaag agataaacc

19

<210> 81
<211> 19
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<223> upstream amplification primer for SEQ 42, SEQ 63, SEQ 43, SEQ 64, SEQ 44, SEQ 65

<400> 81
gggcttctta tggtctttc

19

<210> 82
<211> 20
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<220>
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<223> upstream amplification primer for SEQ 45, SEQ 66, SEQ 46, SEQ 67

<400> 82
gcctaaaaaa acgctgaaag

20

<210> 83
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
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<223> upstream amplification primer for SEQ 47, SEQ 68

<400> 83
tagtaagttc tgtgacaac

19

<210> 84
<211> 18
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<223> upstream amplification primer for SEQ 48, SEQ 69

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gtttggtctc ccttttcc

18

<210> 85
<211> 20

<212> DNA
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<220>
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<223> upstream amplification primer for SEQ 49, SEQ 70

<400> 85
caaaagaaac tcacaaagac 20

<210> 86
<211> 18
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<220>
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<222> 1..18
<223> upstream amplification primer for SEQ 50, SEQ 71

<400> 86
tctggtattt gggaacac 18

<210> 87
<211> 19
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<220>
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<223> downstream amplification primer for SEQ 30, SEQ 51

<400> 87
gtggaaagat aaaatccag 19

<210> 88
<211> 19
<212> DNA
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<220>
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<223> downstream amplification primer for SEQ 31, SEQ 52

<400> 88
caagattttg cctttcctg 19

<210> 89
<211> 19
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<220>
<221> primer_bind

<222> 1..19
<223> downstream amplification primer for SEQ 32, SEQ 53

<400> 89
gaaaaaacagt gactctttg 19

<210> 90
<211> 19
<212> DNA
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<220>
<221> primer_bind
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<223> downstream amplification primer for SEQ 33, SEQ 54

<400> 90
aataaaggtc acaaggaac 19

<210> 91
<211> 20
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<223> downstream amplification primer for SEQ 34, SEQ 55, SEQ 35, SEQ 56

<400> 91
atgaggatct caaatacaag 20

<210> 92
<211> 19
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<220>
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<223> downstream amplification primer for SEQ 36, SEQ 57

<400> 92
gctatcaaat tcctcattc 19

<210> 93
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<220>
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<223> downstream amplification primer for SEQ 37, SEQ 58

<400> 93
cacaaaaact ttcttcacag 20

<210> 94
<211> 19
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<220>
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<223> downstream amplification primer for SEQ 38, SEQ 59, SEQ 39, SEQ 60, SEQ 40, SEQ 61

<400> 94
ttccctagaa aaagatcag 19

<210> 95
<211> 19
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<223> downstream amplification primer for SEQ 41, SEQ 62

<400> 95
caaatttcta tcagtaggg 19

<210> 96
<211> 20
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<223> downstream amplification primer for SEQ 42, SEQ 63, SEQ 43, SEQ 64, SEQ 44, SEQ 65

<400> 96
acagtagttg gtaatgtcac 20

<210> 97
<211> 18
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<220>
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<222> 1..18
<223> downstream amplification primer for SEQ 45, SEQ 66, SEQ 46, SEQ 67

<400> 97
agcaacacta tccacctc 18

<210> 98
<211> 20

<212> DNA
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<400> 98
gtttttttaa gcaagtagcc 20

<210> 99
<211> 20
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<220>
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<223> downstream amplification primer for SEQ 48, SEQ 69

<400> 99
aaagcctcca tttgccacag 20

<210> 100
<211> 21
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<223> downstream amplification primer for SEQ 49, SEQ 70

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attctcattc tctcattttc c 21

<210> 101
<211> 19
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<222> 1..19
<223> downstream amplification primer for SEQ 50, SEQ 71

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aataaaggtc acaaggaac 19

<210> 102
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<222> 1..19
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<400> 102
actttcttaat accctagat 19

<210> 103
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<223> microsequencing oligo for 5-127-261.mis1

<400> 103
gtatacaaga gtttaattt 19

<210> 104
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<400> 104
tgcttggtg tgctccac 19

<210> 105
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<400> 105
ctcttataat taaaaaaaaa 19

<210> 106
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<223> microsequencing oligo for 5-130-257.mis1

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<210> 107
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<220>
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<400> 107
ataatagcag tgaagaaga 19

<210> 108
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<210> 109
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<212> DNA
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<210> 110
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<210> 111
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<210> 112
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<210> 114
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<210> 118
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<400> 118
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<210> 119
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<210> 120

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<211> 19
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<400> 120
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<400> 121
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<210> 123
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<400> 123
aawccagtaa cagtaataa 19

<210> 124
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<400> 124
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<400> 125
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<220>
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<222> 1..19

<223> potential microsequencing oligo for 5-145-24.mis2

<400> 133

acatgttctt tatgacatt

19

<210> 134

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<222> 1..19

<223> potential microsequencing oligo for 5-148-352.mis2

<400> 134

attcccagac aagttggaa

19

<210> 135

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agtgttcggc acaaattaa

19

<210> 136

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27

<210> 138

<211> 30

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<223> sequencing oligonucleotide PrimerRP

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caggaaacag ctatgacc

18

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